DSP-12, 1656 Base Pairs

AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGGA**TG**GTTCTCCGACTGTGGAGCGAC CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT CGATAATTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC TTAGGGCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG CGGCTCCTTGCTGCAGGTGGAGGAGGACGGAAAGGGAGGAGGGCCTGGGAGCAGGAGGT GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGGTGATTCTGCTGGTGGGTACG TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT AΑ

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY HFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF FYCLLWAPSSHLQGPEGSFTG

The second secon

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA ${\tt AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC} \textbf{ATG} \texttt{ACCCTGAGCACGTTGGCCCGC}$ AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC ATTTGGATGGTGATGGTGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG CATAACTACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAGAAGACGAACGGT AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGT CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT TTCTCATCCTTACCTGACCCCATCTATAAAATGAAAATCAAGAGATCCATCTCACAGGGTTATT

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

A DSP13 Alternate Splice Variant, 723 Base Pairs

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTT AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGATC**ATG**ATGC AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG GAATCTGGACCGAGCCTATGACTATGTGAAAGAAGACGAACGGTAACCAAGCCCAACCCAAGC TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG GAGGGAGGGACAAGCCCTGGGGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG AATGTTTATAAAAAAAAAAAAAAAAAAAAA

B DSP13 Alternate Splice Variant, 241 Amino Acids

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

| 100 | NLSQF NLSQF KLLPH EISBH DISSH DISSH DISSH DLLAH NLSRY LS | | |
|-----|--|----------------------|--|
| 90 | SOLDRO-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCRKDSTNLDVLEFFGIKYILNVTPNLPMLFENRGEFKYKQIPISDHHSQNLSQF DRELPSSATESDGSPVSQPRFPVQILPFLYLGCRKDSTNLDVLEFFGIKYILNVTPNLPMFFEHGGFFFYKQIPISDHHSQNLSQF GLCEGKPROLLPHSCLSQPCLPVPSVGLTRILPHLYLGSGKDVLNKDLHTQNGISYVLNRSNSCPWFFEHGGFFFYKQIPISDHHSQNLSGF GLCEGKPROLLPHSCLSQPCLPVPSVGLTRILPHLYLGSGKDVLNKDLHTQNGISYVLNRSNSCPWFFE-GLFHYKQIPISDHYCEKLLPH PRQRIPPRGRENSNSDPRVPIYDGGPVEILPFLYLGSGYHRSKDHLDRLGITRLNVSRSCPWFFEGHYQYKCIPVEDNUKRDISSH PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSRYHRRRDMLDRLGITRLNVSR | | |
| 80 | PNL FENRGEFKY PNRFEHGGEFYY PNRFEHGGEFYY PNRFE-GLFHY PNRFE-GHYQY PNRFE-GHYQY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY IONFFP-GLFRY | 18#82 | ERTLGLSS ERTLGLSS ERSLRLE ETQVLCH ESQVLRPH ESQVLRTP ESETLPSTP EGILDRSKQ QGTLLRSFL |
| | | 170 | NFMGQLLDFI NFMGQLLDFI NFMGQLLDFI NFLGQLLQFI SFMGQLLQFI SFMGQLLQFI SFMGQLLQFI GFMGQLEFY GFMRQLEFY GFMRQLEFY GFMRQLEFY GFMRQLEFY |
| 99 | GIKYILNYTP GIKYILNYTP GIRYILNYTP GITRYLNYSP GITRLNYSP GITRLNYSP HITRLNYSP GVOYILNYTR GENYTLNYTR GENYTLNYTR GENYTLNYTR | 160 | ANDRYDTVKMKSNISPNFNFMGQLLD LINDRYDFVKRKSNISPNFNFMGQLLD SDDRYRFVKDRRPSISPNFNFLGQLLE LIDERFEFVKQRRSTSPNFSFMGQLLQ LLEERFEFVKQRRSTISPNFSFMGQLLQ LLKERFDYIKQRRSTISPNFSFMGQLLQ LLKRRYNYVKQKRSTIRPNRGFMGQLLQ LDRRYDYVKRKSTIRPNAGFNRQLSE WKSALSIVRQNR-IGPNDGFLRQLCQ ANDRYDYKERTVTKPNPSFNRQLEE |
| 20 | TNLOVLEFFGT TNLOVLEFFGT ANLESLAKLGT LNKDLATQNGJ SDLQGLQACGG SRKDMLDALGG SRKCFLANLHJ SNLEELQGSGA GOTPKLQKLGG | 150 | MADAYDIVK LINDAYDIVK SIDDAYBIVK SIDDAYBIVK ALEENFEFVK KLEENFEFVK KLEENFEFVK ALEKNYNYK MIDRAYDYK MIDRAYDYK ALDRAYDYK ALDRAYDYK ALDRAYDYK ALDRAYDYK |
| | SFPVEIL PFLYLGCRKDSTNLDVLEFFGIKYIL NVTP—— SFPVQIL PYLYLGCRKDSTNLDVLEFFGIKYIL NVTP—— SFPVQIL PYLYLGSRRDSNLESLRKLGIRYIL NVTP—— VGLTRIL PYLYLGSRRDSNLESLRKLGIRYIL NVTP—— VGLTRIL PYLYLGSRVHRSSDLQGLQRCGITRVLNVSR—— GGPVEIL PFLYLGSRYHRRRDMLDRLGITRLINVSR—— GGPVEIL PFLYLGSRYHRRRDMLDRLGITRLINVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PFLYLGSRYHRSKCFFLRNLHITRLLNVSR—— GGPVEIL PHYLGSELNNSNLEELQGSGVDYIL NVTR—— ODFYTQIFEHVFLGSELNNSNLEDLQNRGVRYIL NVTR—— OPPCNEVTPRIYVGNASVRQDIPKLQKLGITHVLNRREGRS P eilp lylgsa an \$ g! y LNv | 140 150 160 170 1808 | ISRSYTVTVAYLHÖKLNLSKNORYDIVKHKKSNISPNFNFHGOLLDFERTLGLSS ISRSYTVTVAYLHÖKLNLSLNORYDEVKRKKSNISPNFNFHGOLLDFERTLGLSS VSRSYTVTVAYLHÖKNISLNORYDEVKRKKSNISPNFNFHGOLLDFERTLGLSS VSRSYTVTVAYLHÖKNISLNORYDEVKRKKSNISPNFNFHGOLLDFERSLRLE ISRSATICLAYLHÖKNRLDERFDFVKORRSISPNFSFHGOLLQLETQVLCH ISRSATICLAYLHKRAYLLERFEFVKORRSISPNFSFHGOLLQFESQVLAPP ISRSATICLAYLHKRKAYLERFEFVKORRSISPNFSFHGOLLQFESQVLAPS VSRSASTVIAYAHKRYCHLEKAYNYKOKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRYKHOVRLERAYNYKOKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRAYLHKRAYLKATVIKANYKKRSITRPNAGFHROLSEYEGILDASKQ VSRSASTVIAYAHKRAYLHKRAYLHKAYLAYAYVKOKRSITRPNAGFHROLSEYEGILDASKG VSRSASTVIAYAHKRAYLHKRAYLAYAVAYAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLYAYLAYAVAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLAYAVAYAKRRIVIKPNPSFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLASFL VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYGILLANFKG VSRSASTVIAYLHKRAYLAYAVAKAKRSITRPNAGFHROLSEYAGILDAKA INTAKKA INTA |
| 99 | SOLORD-PHSATOSOGSPLSNSQPSFPVEILPFLYLGCRKDSTNLOVLEEFGIKYILNVTP DRELPSSATESOGSPVPSSQPRFPVQILPYLYLGCRKDSTNLOVLEEFGIKYILNVTP GATPPPVGLRASFPVQILPNLYLGSRRDSANLESLAKLGIRYILNVTP GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKOLMTQNGISYVLNASN PAQALPPAGAENSNSDPRVPTYDQGGPVEILPFLYLGSRYHASRKDMLDALGITALLNVSA PVPPSATEPLOLGCSSCGTPLHDQGGPVEILPFLYLGSAYHASRKDMLDALGITALLNVSA SERALISQCGKPVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCFFLANLHITALLNVSS GANCOLKELKEFIDNEMLILGQADSPTQIFFHYLGSAYHASKCFFLANLHITALLNVSR QANCOLREFKEFIDNEMLYILGQADSPTQIFFHYLGSEWNASNLEDLQNRGVRYILNVTR GANCOLREFKEFIDNEMILYLGQADSPTQIFFHYLGSEWNASNLEDLQNRGVRYILNVTR | 130 | FPERISFIDER-RGKNCGVLYHCLRGISRSYTYTYRYLHQKLNLSKNDRYDTVKHKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-RSKKCGVLYHCLRGISRSYTYTYRYLHQKLNLSLNDRYDFVKRKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-LSQUCGVLYHCLRGISRSYTYTYRYLHQKLNLSLNDRYDFVKRKKSNISPNFNFNGQLLDFERTLGLSS FPERISFIDER-LSGQVLYHCLRGISRSRTIRITRIANTHKHRSSDDRYRFVKDRRFSISPNFNFLGGLLEYERTLKLR FRENISFIDSY-KNSGGRVLYHCQRGISRSRTICLRYLHRKKVRLDERFDFVKQRRGVISPNFSFNGQLLQLETQVLCH FNERIDFIDSI-KNRGGRVLYHCQRGISRSRTICLRYLHRKKWRLEERFFFVKQRRSIISPNFSFNGQLLQFESQVLRTF FQERIDFIDCY-REKGGRVLYHCGRGISRSPTICHRYLHKKKVRLEERFFFVKQRRSIISPNFSFNGQLLQFESQVLRTS HNERYHFINKR-KRNHSKLYHCKHGVSRSRSTVIRYRMKFFGHPLEKRYNYVKQKRSIIRPNRGFNRQLSEYEGILDRSKQ HNDTYKFISKR-KHGSKLYHCKHGVSRSRSTVIRYRMKFFGHNUDRRYVKQKRSIIRPNRGFNRQLSEYEGILDRSF FRANDFIDGALQKNGRVLYHCREGYSRSPTLVIRYLHRRQKNOVKSRLSTVRQNRE-IGPNDGFLRQLCQLNDRLRKG F eai FI# a k v1YHC aGISRSAL IRYIH 1 Ay ! kqrr ispNf F\$gQLL## 1 |
| 50 | SOGSPLSNSOP GATPPPVGLRR GATPPPVGLRR ASLSQPCLPVPS SNSDPRVPTYDQ GCSCCTPLHDQ VVNVSYRPRYDQ TONEMLLILGQH LSDGSGCYSLPS | 120 | KNCGVL VHCLAG KKCGVL VHCLAG SCGVL VHCLAG SCGVL VHCQAG GCGRVF VHCQAG CRGRVL VHCQAG KGGRVL VHCQAG KGGRVL VHCQAG KGGRVL VHCQAG NISKCL VHCKAG VIVHC AG |
| 10 | SOLORO-PNSATOSOGSPLSNSQP DRELPSSATESOGSPLSNSQP GATPPYGLRA GLCEGKPAALLPMSLSQPCLPVPS PADALPPAGAENSNSDPRVPIYDQ PLSTSVPDSAESGCSSCGTPLYDQ PVPPSATEPLOLGCSSCGTPLHOQ SERALISQCGKPVNVSYRPAYDQ QMNCNLKELKEFIDNENLLILGQH QMVCNLREFKEFIDNENLLILGQH | 110 110 | FPERISFIDER-RGKNCGVLVHCLNG FPERISFIDER-LSGNCGVLVHCLNG FPERIFFIDER-LSGNCGVLVHCLNG LDKSIEFIDKR-KLSSCQVIVHCLNG FQERISFIDSV-KNGGGRVFVHCQNG FNERIDFIDSV-REKGGKVLVHCQNG FNERIDFIDCV-REKGGKVLVHCCNG HNERYHFINKR-KRNISKCLVHCKNG FRANDFIDGALAQKNGRVLVHCKNG FERANDFIDGALAQKNGRVLVHCKG |
| ₩- | | 101 | |
| | PYST1 MKP-7 MKP-4, hVH5 PRC1 MKP-2, MKP-5, MKP-5, MKP-12 OSP-12 OSP-12 | | PYST1 MKP-7, MVH5 PRC1 MKP-2, MKP-2, MKP-2, MKP-2, MKP-12 DSP-12 DSP-13 |

Figure 6

Alignment of DSP-12 and DSP-13

| 110 |
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| 100 |
| 96 |
| 80 |
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OSP-13 MTLSTLARKRKAPLACTCSLGGPOMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHAGOLQQHLQAAFILLRPEONIRLAVRLESTYQNR

| 220 1 YESCI YESHI |
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| 111 120 130 140 150 160 170 180 190 200 210 220 10 10 10 10 10 10 10 10 10 10 10 10 10 |
| 200 RCEVARRHNYF RCEVARAHNYY |
| 190 HSALQVLHKI |
| 180 IIFKPVSVQARIIFKPVSVQAR |
| 170 FSVSTNGRHI FSVSTDNRVF |
| 160 TKTHLUGDGG |
| 150 HYLRLHSD HGLYLPLHSD |
| 140 + FSSNDSSTCT |
| 111 120 130 140 |
| 120 + |
| 111 |
| 0SP-12 0SP-13 |

| 330 LGSEHNA LGSEHNA |
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| 320 PSLIFOHLY PTQIFEHVF |
| 310 HLILGONDK HIVILGONDS |
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| 270 RSTHMSQOLE REIMAQKOLE |
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| 221 230 240 250 250 280 290 300 310 320 330 330 330 330 330 330 330 330 33 |
| 221 1 SSE09 NSD05 |
| 0SP-12 0SP-13 |

| 440 SITRPNN TVTKPNP |
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| 430 KRYNYVKÜKR RRYDYVKERR |
| 420 AMKEFGUPLE AMKEYGUNLD |
| 410 SRSASTVIAYI SRSASTVIAYI |
| 400 CCLVHCKHGVS CCLVHCKHGVS |
| 390 TINKUKRNIISK TISKAKKHGSK |
| 380 LAHIMHERYH |
| 360 370 380 390 400 410 420 430 440 31 FAYINIRVYDEETTDLL RIUNHERYIIF INKOKRNIISKCLYHCKHGVSRSASTVIRYRHKEFGUPLEKRYNVKQKRSITRPNN 31 FAYINIRVYDEENTDLL RYWNDI YKFISKRKHGSKCLYHCKHGVSRSASTVIRYRHKEYGUNLDRRYDYVKERRIVIKPNP |
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| 490 YGDFLPETPDO |
| 480 9-gpvddprgi EFESVOLVSI |
| 470 LURQQTDSSL RDKPUGEKSTI |
| 441 450 460 470 480 490 500 510 520 530 540 550 550 550 550 550 550 550 550 55 |
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| 441 GFHR0 SFHR0 |
| DSP-12 DSP-13 |

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| | 200 | | EAAPPAEYHRPARUPQQGSGLCEKDVI |
| | 551 | | □ |
| | | | DSP-12 |

